

**CLAIMS**

1. A method of producing a lipolytic enzyme variant comprising:
  - a) selecting a substrate and an ester bond of interest,
  - b) selecting a parent lipolytic enzyme having an alcohol binding site having a glycerol part with an sn2 position,  
5
  - c) in the parent lipolytic enzyme selecting at least one amino acid residue which comprises at least one atom within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride in a three-dimensional structure of the parent lipolytic enzyme and the substrate,
  - d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,  
10
  - e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),
  - f) preparing the variant resulting from steps b-d,
  - 15
  - g) testing the activity of the variant on the selected ester bond,
  - h) selecting a variant having an altered activity on the selected ester bond, and
  - i) producing the selected variant.
2. A method of producing a lipolytic enzyme variant comprising:  
20
  - a) selecting a substrate and an ester bond of interest,
  - b) selecting a parent lipolytic enzyme having a structure comprising a catalytic triad consisting of an active Ser, an active Asp and an active His residue,
  - c) in the parent lipolytic enzyme selecting at least one amino acid residue comprising at least one atom belonging to a set E defined by the following  
25 steps:
    - i) aligning the structure of the lipolytic enzyme with *Rhizomucor miehei* lipase structure 4TGL comprising a catalytic triad and an inhibitor phosphorus atom (4TGL-inhP), so as to minimize the sum of squares

- of deviation between atoms of the catalytic triads of the two structures,
- ii) defining a set A consisting of atoms of the lipolytic enzyme inside a sphere of radius 18 Å with center at 4TGL-inhP,
- 5 iii) forming a first plane defined by 4TGL-inhP, the C<sub>α</sub> atom of the active Ser residue of the parent lipolytic enzyme, and the C<sub>α</sub> atom of the active Asp residue of the parent lipolytic enzyme and defining a set B as a subset of set A consisting of atoms on the same side of the first plane as the C<sub>α</sub> atom of the active His residue of the parent lipolytic enzyme,
- 10 iv) forming a second plane defined by 4TGL-inhP, the C<sub>α</sub> atom of the active Ser residue of the parent lipolytic enzyme, and the C<sub>α</sub> atom of the active His residue of the parent lipolytic enzyme and defining a set C as a subset of set A consisting of atoms on the opposite side of the second plane from the C<sub>α</sub> atom of the active Asp residue of the parent lipolytic enzyme,
- 15 v) forming a set D consisting of atoms belonging to the union of sets B and C, and having a solvent accessibility of 15 or higher, and
- vi) forming set E consisting of amino acid residues in the structure which comprise an atom belonging to set D or an atom belonging to the union of sets B and C and located less than 3.5 Å from an atom belonging to set D,
- 20
- d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,
- e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than d),
- f) preparing the variant resulting from steps d) - f), and
- g) testing the activity of the variant on the selected ester bond,
- h) selecting a variant having an altered activity on the selected ester bond,
- 25 and
- i) producing the selected variant.

3. A method of producing a lipolytic enzyme variant comprising:
- a) selecting a substrate and an ester bond of interest,
  - b) selecting a parent lipolytic enzyme having an active site comprising an active His residue,
  - 5 c) in the amino acid sequence of the parent lipolytic enzyme selecting at least one amino acid residue at the C-terminal side of the active His residue,
  - d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,
  - e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),
  - 10 f) preparing the variant resulting from steps b-d,
  - g) testing the activity of the variant on the selected ester bond,
  - h) selecting a variant having an altered activity on the selected ester bond, and
  - 15 i) producing the selected variant.

4. A method of producing a lipolytic enzyme variant comprising:
- a) selecting a substrate and an ester bond of interest,
  - b) selecting a parent lipolytic enzyme,
  - c) selecting at least one amino acid residue among 10 amino acid residues at the C-terminal,
  - 20 d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,
  - e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),
  - f) preparing the variant resulting from steps c) - e),
  - 25 g) testing the activity of the variant on the selected ester bond,
  - h) selecting a variant having an altered activity on the selected ester bond, and
  - i) producing the selected variant.

- 30 5. A method of producing a lipolytic enzyme variant comprising:

- 5
- a) selecting a substrate and an ester bond of interest,  
b) selecting a parent lipolytic enzyme having a lid,  
c) selecting at least one amino acid residue in the lid,  
d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,  
e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),  
f) preparing the variant resulting from steps c) - e),  
g) testing the activity of the variant on the selected ester bond,  
10 h) selecting a variant having an altered activity on the selected ester bond, and  
i) producing the selected variant.

15 6. The method of any of claims 1-5 wherein the lipolytic enzyme is native to an eukaryote, preferably to a fungus, and most preferably belongs to the *Humicola* family or the *Zygomycetes* family.

7. A method of producing a lipolytic enzyme variant comprising:
- 20 a) selecting a substrate and an ester bond of interest,  
b) selecting a parent lipolytic enzyme from the *Humicola* family or the *Zygomycetes* family,  
c) selecting at least one amino acid residue corresponding to any of amino acids 20-25, 56-64, 81-85 and 255-269 in the *Humicola lanuginosa* lipase  
25 d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,  
e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),  
f) preparing the variant resulting from steps b-e,  
g) testing the activity of the variant on the ester bond in the substrate, and  
h) selecting a variant having an altered activity on the ester bond.

8. The method of claim 7 wherein the parent lipolytic enzyme is the lipase of *Humicola lanuginosa* strain DSM 4109.
9. The method of any of claims 1-8 wherein the altered activity is a lower activity towards a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride, or a lower ratio of activity towards a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride and a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride.
10. The method of claim 9 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.
11. The method of any of claims 1-8 wherein the altered activity is a lower activity towards a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride, or a lower ratio of activity towards a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride and a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride.
12. The method of any of claims 1-8 wherein the altered activity is a higher phospholipase activity.
13. The method of claim 12 wherein the parent lipolytic enzyme has a phospholipase activity below 50 PHLU/mg and/or a ratio of phospholipase activity to lipase activity below 0,1 PHLU/LU.
14. The method of claim 12 or 13 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to R81, R84, S85, or 263-267 (e.g. G266 or T267) in the *Humicola lanuginosa* lipase.
15. The method of any of claims 12-14 wherein the alterations comprise insertion of a peptide extension at the C-terminal, preferably comprising 1-5 amino acid residues, the first preferably being A, P or D, the second (if present) preferably being V, G or

R, the third (if present) preferably being V, G or R, the fourth (if present) preferably being F, and the fifth (if present) preferably being S.

16. The method of any of claims 1-8 wherein the altered activity is a higher hydrolytic activity on a digalactosyl-diglyceride.

5 17. The method of claim 16 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to 21, 23, 26, 57, 62, 81, 83, 84, 85, 266, 267 or 269 in the *Humicola lanuginosa* lipase.

10 18. A method of preparing a lipolytic enzyme variant for use in baking, which method comprises:

- a) selecting a parent lipolytic enzyme,
- b) making at least one alteration which is an insertion, a deletion or a substitution of an amino acid residue in the lipolytic enzyme to obtain a lipolytic enzyme variant,
- c) screening for a lipolytic enzyme variant which compared to the parent lipolytic enzyme has
  - i) a higher ratio selectivity for long-chain fatty acyl groups,
  - ii) a higher activity on digalactosyl diglyceride, and
  - iii) a higher phospholipase activity, and
- d) preparing the lipolytic enzyme variant.

19. The method of claim 18 wherein the parent lipolytic enzyme and the amino acid to be altered are selected as defined in any of claims 1-8.

20. A method of preparing a lipolytic enzyme variant for use in baking, which method comprises

- a) subjecting a DNA sequence encoding a lipolytic enzyme to random mutagenesis,

- b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and
- c) screening for host cells expressing a lipolytic enzyme variant which compared to the parent lipolytic enzyme has:
- 5 i) a higher ratio selectivity for long-chain fatty acyl groups,
- ii) a higher activity on digalactosyl diglyceride, and
- iii) a higher phospholipase activity, and
- d) preparing the lipolytic enzyme expressed by the host cells.

21. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having an alcohol binding site having a glycerol part with an sn2 position, which variant:

- 10 a) comprises an alteration which is an insertion, a deletion or a substitution of an amino acid residue, at a position which in a three-dimensional structure of the parent lipolytic enzyme and a substrate is within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride, and
- 15 b) has an altered activity on an ester bond in the substrate.

22. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having a lid, which variant:

- 20 a) comprises an alteration which is an insertion, a deletion or a substitution of an amino acid residue in the lid,
- b) has an altered activity on an ester bond in the substrate.

23. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having an active site comprising an active His residue, which variant:

- 25 a) comprises an alteration which is an insertion, a deletion or a substitution of at least one amino acid residue at the C-terminal side of the active His residue,
- b) has an altered activity on an ester bond in a substrate.

24. A lipolytic enzyme which is a variant of a parent lipolytic enzyme, which variant:

62

- a) comprises an alteration which substitution of at least one amino acid residue of the C-terminal, is an insertion, a deletion or a acid within 10 amino acid residues of the C-terminal,
- b) has an altered activity on an ester bond in a substrate.
- 5 25. The lipolytic enzyme of any of claims 21-24 wherein the parent lipolytic enzyme is native to an eukaryote, preferably to a fungus, and most preferably belongs to the *Zygomycetes* family.
26. The lipolytic enzyme of claim 25 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109.
- 10 27. A lipolytic enzyme which:
- a) is a polypeptide having an amino acid sequence which has at least 80 % homology with a reference lipolytic enzyme of the *Humicola* family or the *Zygomycetes* family;
- 15 b) compared to said reference lipolytic enzyme comprises an amino acid alteration which is:
- i) a substitution, deletion or insertion at a position corresponding to A20, Y21, G23, K24, N25, V63, R81, G82, R84, A257, W260, Y261, F262 or G266 in the *Humicola lanuginosa* DSM 4109 lipase;
- 20 ii) a substitution of an amino acid corresponding to C268 or L269 in said lipase;
- iii) a substitution corresponding to V60G, D62E, L93K, L97Q, K98E,F, E99D, P256A, G263E,Q,R,F,N, L264A,C,P,F,G,V,I, I265L,N,F or T267A,Q,P,S,V,E in said lipase;
- 25 iv) an insertion corresponding to T267GS or T267GL in said lipase;
- v) a peptide extension at the C-terminal which is A, P, MD, CP, AG, DG, AGG, PVGF, AGRF, PRGF, AGGF or AGGFS;
- vi) a peptide extension at the C-terminal of 40-50 amino acids; or

63

- vii) a truncation of 1, 2, 3, 4, 5 or 6 amino acids at the C-terminal; and
- c) has an altered activity on an ester bond in a substrate compared with the reference lipolytic enzyme.
- 5 28. The lipolytic enzyme of claim 27 wherein the amino acid alteration corresponds to R84K,L,W, W260H,Q,C, G266A,C,D,N,L,I,S,T,P,V,F,W,E,K,R,Y or L269N,I,S.
29. The lipolytic enzyme of claim 27 or 28 which further comprises at least one further amino acid alteration which is a substitution, a deletion or an insertion corresponding to any of positions 22, 56-59, 61, 64, 83, 85, 91, 94, 249, 255 or 259  
10 preferably S83T, G91A, N94D, D96S,W,F,G, Q249R or L259N,R,S,M,Q.
30. The lipolytic enzyme of any of claims 27-29 which further comprises a substitution corresponding to D62A,G,V, K98D, E99K, P256T, G263A and/or I265T,G,V.
31. The lipolytic enzyme of any of claims 27-30 which comprises a peptide extension at the N-terminal.
- 15 32. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Humicola lanuginosa*.
33. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Rhizomucor miehei*.
- 20 34. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Fusarium oxysporum*.
35. A lipolytic enzyme which:
- a) is a polypeptide having an amino acid sequence which has at least 80 % homology with a reference enzyme which is the lysophospholipase from *Aspergillus foetidus*, the ferulic acid esterase from *Aspergillus niger*, the ferulic

acid esterase from *Aspergillus* *tubigensis* or phospholipase A1 from *Aspergillus oryzae*,

- b) compared to said reference enzyme comprises an amino acid alteration which is a substitution, deletion or insertion at a position corresponding to 20-5, 25, 56-64, 81-85, 91-98, 255-257 or 259-269 in the *Humicola lanuginosa* lipase, and  
c) has an altered activity on an ester bond in a substrate compared with the reference enzyme.

36. The lipolytic enzyme of claim 35 wherein the alteration is at a position corresponding to Y21, E56, D57, V60, G61, D62, S83, R84, G91, L93, N94, D96, L97, K98, E99, P256, W260, Y261, G263, L264, I265, G266, T267 or L269 in the *Humicola lanuginosa* lipase

37. The lipolytic enzyme of claim 35 or 36 wherein the alteration is an extension or a truncation at the C-terminal, preferably by 1-5 amino acids.

38. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a lower activity towards a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride, or a lower ratio of activity towards a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride and a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride.

39. The lipolytic enzyme of claim 38 which comprises an amino acid alteration at a position corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.

40. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a lower activity towards a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride, or a lower ratio of activity towards a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride and a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride.

41. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a higher phospholipase activity.

42. The lipolytic enzyme of claim 41 which comprises an amino acid alteration at a position corresponding to R81, R84, S85, G263, L264, I265, G266, T267 or L269 in the *Humicola lanuginosa* lipase, preferably a substitution corresponding to G263A,E,Q,R; L264A,C,P,Q; I265L,N,T; G266A, C, D, N, L, I, S, T, P, V or T267A,Q or L269N.
43. The lipolytic enzyme of claims 41 or 42 which has a phospholipase activity greater than 0.1 nmol/min in a monolayer assay at pH 5 as described herein and/or a phospholipase activity greater than 100 PHLU/mg (preferably greater than 500 PHLU/mg) and/or a ratio of phospholipase activity to lipase activity greater than 0.1 PHLU/LU (preferably greater than 0.5 PHLU/LU).
44. The lipolytic enzyme of any of claims 41-43 wherein the parent lipolytic enzyme has a phospholipase activity below 50 PHLU/mg and/or a ratio of phospholipase activity to lipase activity below 0.1 PHLU/LU.
45. The lipolytic enzyme of any of claims 41-44 which comprises a peptide extension at the C-terminal, preferably comprising 1-5 amino acid residues, the first preferably being A, P or D, the second (if present) preferably being V, G or R, the third (if present) preferably being V, G or R, the fourth (if present) preferably being F, and the fifth (if present) preferably being S.
46. The lipolytic enzyme of any of claims 41-45 which comprises a deletion of amino acid residues at positions corresponding to positions C268 and L269 in the lipase of *Humicola lanuginosa* strain DSM 4109.
47. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a higher hydrolytic activity on a digalactosyl-diglyceride.
48. The lipolytic enzyme of claim 47 which comprises an amino acid alteration at a position corresponding to Y21, G23, N26, D57, D62, R81, S83, R84, S85, G266, T267 or L269 in the *Humicola lanuginosa* lipase, preferably comprising two or more

such alterations, most preferably further comprising at least one alteration in the lid region

49. The lipolytic enzyme of any of claims 27-48 which comprises an alteration in the lid which is a substitution of a negatively charged amino acid residue with a neutral or 5 positively charged amino acid residue, or a substitution of a neutral amino acid residue with a positively charged amino residue.
50. The lipolytic enzyme of claim 49 which comprises an alteration in the lid at a position corresponding to position G91, D96 and/or E99 in the *Humicola lanuginosa* lipase, preferably a substitution which is G91A, D96S,W,F or E99K.
- 10 51. A lipolytic enzyme which is a variant of a parent lipase derived from *Humicola lanuginosa* strain DSM 4109 comprising the alterations E1E,D,A+ G91G,A,S,T+ N94N,D+ D96D,G,F,W+ E99E,K+ G225G,R,K+ G263Q,N+ L264L,A,V+ I265I,T,S+ G266G,A,V,S,D,E+ T267T,A,V+ L269L,I,N,Q
- 15 52. The lipolytic enzyme of claim 51 which further comprises SPIRR as a peptide extension at the N-terminal and/or AGGF or AGGFS as a peptide extension at the C-terminal.
53. A DNA sequence encoding the lipolytic enzyme of any of claims 27-52.
54. A vector comprising the DNA sequence of claim 53.
- 20 55. A transformed host cell harboring the DNA sequence of claim 53 or the vector of claim 54.
56. A method of producing the lipolytic enzyme of any of claims 27-52 comprising  
a) cultivating the cell of claim 55 so as to express and preferably secrete the lipolytic enzyme, and  
b) recovering the lipolytic enzyme.

57. A process for preparing a dough or a baked product prepared from the dough which comprises adding the lipolytic enzyme of any of claims 27-52 to the dough, wherein the lipolytic enzyme preferably has phospholipase and/or digalactosyl diglyceride activity.
- 5 58. The process of claim 57 which further comprises adding to the dough an endo-amylase and/or a phospholipid.
59. The process of claim 57 or 58 wherein the endo-amylase is from *Bacillus*, and is preferably a maltogenic amylase from *B. stearothermophilus*,
- 10 60. A process for reducing the content of phospholipid in an edible oil, comprising treating the oil with the lipolytic enzyme of any of claims 41-46, 51 or 52 so as to hydrolyze a major part of the phospholipid, and separating an aqueous phase containing the hydrolyzed phospholipid from the oil.
- 15 61. A process for improving the filterability of an aqueous solution or slurry of carbohydrate origin which contains phospholipid, which process comprises treating the solution or slurry with the lipolytic enzyme of any of claims 41-46, 51 or 52, wherein the solution or slurry preferably contains a starch hydrolysate, particularly a wheat starch hydrolysate.
- 20 62. A detergent composition comprising a surfactant and the lipolytic enzyme of any of claims 27-52, wherein the lipolytic enzyme preferably has a specificity for long-chain fatty acids corresponding to a ratio of SLU to LU above 3.
- 25 63. A method of enhancing the flavor of a food product containing milk fat, comprising treating the food product with the lipolytic enzyme of any of claims 27-52 so as to release free fatty acids, wherein the lipolytic enzyme preferably has a specificity for short-chain fatty acids corresponding to a ratio of SLU to LU below 0.5, more preferably below 0.2, e.g. below 0.1.

64. A method of preparing a dough or a baked product prepared from the dough, comprising:

- a) testing at least one lipolytic enzyme for its hydrolytic activity towards a C<sub>4</sub>-C<sub>8</sub> acyl bond in a triglyceride, a C<sub>16</sub>-C<sub>20</sub> acyl bond in a triglyceride, digalactosyl diglyceride and a phospholipid,  
5
- b) selecting a lipolytic enzyme having hydrolytic activity towards digalactosyl diglyceride and the phospholipid, and having a ratio of activity towards the C<sub>16</sub>-C<sub>20</sub> acyl bond and the C<sub>4</sub>-C<sub>8</sub> acyl bond which corresponds to a SLU/LU ratio of at least 3, and  
10
- c) adding the selected lipolytic enzyme to the dough.

MDB  
AL